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FIG. 1A**SUBSTITUTE SHEET (RULE 26)**

1 ACCCTGAGTA GAGCTTGAA AAGTTGAGCC CTCCTCGAGA GAAATTGGAA GAACAGTGTAA AGAGGCTGCT ATTCCAAAA GCTTTCACAT CTCAGCAGTT
 TGGACTCATT CTCGAACCT TTCAACTCGG GAGAAGCTCT CTATAACCTT CTGTCAAT TCTCCGACGA TAGGTTTT CGAAAGTGTAA GAGTGTCAA

101 AGTTTATGTC ATTGTCAATT ACCTGTTCA ACTTATCAC CTTCTGACT TTAGCAATGA AACCAGCGAG CAACATATA GCCAAGATGA GCGCTATGT
 TCAAGTACAG TAACAGTAAT TGACAAGT TGAAAGTAGTG GAGGACTGA ATTCGTTACT TTGGCTCGTC GTGGAATAAT CGGTTCCTACT CGTCGATACA
 MetSer PheLeuGlyIle LeuCysLys CysProLeu GlnAsnGluSer GlnGluGlu SerTyraSer AlaTy-ProLeu

+3 TGGACACACT TGCTGGCCCT CTTTATGCT TTCTCTGGCA TCCTCTGCCA GTGTCCTCTA CAGAATGAGT CTCAGGAGGA GTCTCTACAT GCCTATCCTC
 ACCCTGTCAC ACGACCGGA GAAATACAGA AAAGAACCGT AGGACACGT CACAGGAGAT GTCTACTCA GAGGATGTTA CGGATAGGA

101 LeuProlAlaVal LysValSer MetAspTrpLeu ArgLeuArg ProArgVal PheGlnGluAla ValValAsp GluArgGln TyrIleIlePro TripleUle

+3 TTCCAGCAGT CAAGGTCTCC ATGGACTCGC TAAGACTCG TACCTGAGG TACCTGACCG ATTCTGAGTC TTGGTCCCAG AAAGTCCTCC GTCACACCT ATGTAACCG GGACCACTA

+3 IleSerLeuLeu AsnSerPheHis ProHisGlu GluAspLeu SerSerIleSer AlaThrPro LeuProGlu GluPheGluLeu GluGlyPhe LeuAlaLeu

101 TTCTCTCTG AATAGTTCC ATCCCCATGA AGAGGACCTC TCAAGTATA GTGGCACACC ACTTCAGAG GAGTTGAAT TACAGGATT TTGGCATG
 AAGGAGAGC TTATCCTAAGG TAGGGTACT TCTCCCTGGAG AGTTCTAT CACGCTGTGG TGAAAGTCTC CTCAAACCTA ATGTTCTTA AAACCGTAAC

+3 ArgProSerPhe ArgAsnLeu AspPheSer LysGlyHisGln GlyIleThr GlyAspLys GluglyGlnGln ArgGlnGln ArgArgIleSer

101 AGACCTCTT TCAGGAACCTT GGATTTTCC AAAGGTCACT AGGGTATTAC AGGGGACAAA GAAGGCCAGC AACGACGAAAT AGGACGCAAT CGCTGATCT
 TCTGGAGAGA AGTCTGTGAA CCTAAAAAGG TTTCAGTGG TCCCTATATG TCCCTCTGTT CTTCGGCTG TTGCTGCTTA TGCTGTGTT GCGAACTAGA

+3 SerIleGlyLys TripleAla AspAsnGlnPro ArgLeuIle GlnCysGlu AsnGluValGly LysLeuLeu PheIleProGlu LeuIleLeu

101 CTATAGGCCAA ATCGATTGCT GATAATCAGC CAAGGTGAT TCACTGTGAA AATGAGCTAG GGAAATTGTT GTTTATCACA GAAATCCAG AATTAACT
 GATATCCGTT TACCTAACGA CTATTAGTCG GTTCCGACTA AGTCACACTT TTACTCCATC CTTAGGGTC TTAAATTGTA

+3 LeuGluAspPro SerGluAlaLys GluAsnLeu IleLeuGln GluThrSerVal IleGluSer LeuAlaAla AspGlySerPro GlyLeuLys SerValLeu

101 GGAAGACCCCC AGTGAAGCCA AAGAGAACCT CATTCTGCAA GAAACATCTG TGATAGAGTC GCTGGCTGCA GATGGGAGCC CAGGGCTAAA ATGAGCTGCTA
 CCTTCTGGGG TCACCTGGT TTCTCTGGT GTAGAGCTG ACTATCTGAC CTTCTGAGT CTTCTGAGT GTCCCGATTT TAGTCAGAT

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FIG. 1B**SUBSTITUTE SHEET (RULE 126)**

+3 SerThrSerArg AsnLeuSer AsnAsnCys AspThrGlyGlu LysProVal ValThrPhe LysGluAsnile LysThrArg GluValAsn ArgAspGlnGly

801 TCTACAGCC GAAATTAAAG CAACAACTGT GACACAGGAG AGAACGCCAGT GGTAACCTTC AAAGAAAACA TTAAAGACAGC AGAAGTGAAC AGAGACCAAG AGATGTTGG CTTAAATTCT GTGTGTCGCA CTGTGGTGCAC

+3 GlyArgSerPhe ProProLys GluValArgArg AspTyrSer LysGlyLle ThrValThrLys AsnAspGly LysLysAsp AsnAsnLysArg LysThrGlu

801 GAAGAAGTT TCCTCCAAA GGGACTATAG CAAAGGAATA ACTCTAACTA AGAATGATGG AAAGAAAGGAC AACAAACAGA CGAACACTGA CTTCTCAA ACCAGGGTTT CTCCACTCTT CCCTGATATC GTTCCCTTAT TCTCATGAT TCTCTACTACC TTTCATGTTCTG TTGTGTGTCT CCCTTGACT

+3 GluThrLysLys CysthrLeuGlu LysGlnAsnVal AlaValGln VallysSer GluThrGluLeu ArgLysThr ProValSer

801 AACCAAGAAA TGCACCTTAG AAAAGTTACA GGAAACAGGA AAGCAGAAATG TGGCAGCTGCA GGTAAGAAATCC CAGACAGAAC TAAGAAAGAC TCCACGCTCT TTGGTCTTT ACCTGGGATC TTTCATGTT CCTGGTCTTAC ACCCTGCTGT CCATTGTTAG . GTCTGCTCTG ATTCTCTTG AGGTACAGA

+3 GluAlaArgLys ThrProVal ThrGlnThr ProThrGlnAla SerAsnSer GlnPhelle ProIleHisIle ProGlyAla PheProPro LeuProSerArg

801 GAAGCCAGAA AAACACCTGT AACTCAACC CCAACTCAAG CAACTAACTC CCAGTCTTC CCCATTCTAC ACCCTGGAGC CTTCCCTCTT CTTCCAGCA CTTCGTCTT TTGTGCA

+3 ArgProGlyphe ProProPro ThryrValle ProProPro ValAlaPhe SerMetGlySer GlytyrSer GlyvalserVal ProGlyThr

801 GGCCAGGGTT TCCTCCCCCA ACATATGTTA TCCCCTGGCC TGTTGGCATTT TCTATGGCT CAGGTACAC CTTCAGCT GTCTAAGTAG GGCTTAAGTAG TGGGACCTCG GAAGGGAGGA GAAGGGCTGT

+3 ThrPheLeuGln ProThrAlaHis SerProAla GlyAsnGln ValGlnAlaGly LysGlnSer HisIlePro TyrSerGlnGln ArgProSer GlyProGly

801 CTTCTTCAG CCTCACGGTC ACTCTCCAGGC AGGAACCCAG GTGCAAGCTG GGAAACAGTC CCACATTCCT TAAGGCCAGC AACGGCCCTC TGGACCGGG GAAAGAAGTC GGATGTCGAG TGAGAGCTCG TCCTTGGTC CAGGTGCGAC CCTTGTGAG GGTGTAGGA ATGTCGGTGC TTGCGGGAG ACCTGGTCCC

+3 ProMetAsnGln GlyProGln GlnSerGln ProProSerGln GlnProLeu ThrSerLeu ProAlaGlnPro ThrAlaGln SerThrSer GlnLeuGlnVal

801 CCAATGAAACC AGGGACCTCA ACATACACAG CCACCTTCCC AGCAACCCCT TACATCTTA CCAGCTCAGC CAACAGCACA GTCTACAAGC CAGGTGGAGG

1401 GGTTACCTGG TCCTCTGGAGT TGTAGTGTCTC GCTGAGGTC AGTGTGAAAT GCTGAGGG TCCTGGGGGA ATGTGAAAT GCTGAGGTG CAGATGTTG CAGATGTTG CAGATGTTG

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+3	ValGlnAlaLeu ThrGlnGln GlnGlnSerPro ThrLysAla ValProAla LeuGlySer ProProHis HisSerGly PheGlnGlnTyr GlnGlnAla
11501	TTCAGCTCT AACTCAGCA CAACATCCC CTACAAAGC TGTCGGGGT TGGGGAAA GCCGGCTCA CCRACTCGA TTCCAGGAGT ATCAAACAGGC AAGTTCAGA TTGACTCGT GTGTTAGGG GATGTTCG ACACGGCCA AACCCCTTT CGGGGAAGT GETGAGACTT AAGGTGGCA TAGTGTGCC
+3	AlaAspAlaSer LysGlnLeuTrp AsnProPro GlnValGln GlyProLeuGly LysIleMet ProVallys GlnProTyr LeuGlnThr GlnAspPro
11501	AGATGCCCTCC AACAGCGCTG GGAAATCCCTCA TTAGGTCAA GTTCATTAG GGAAATAT GCCTGTAAA CAGGCACTT CCTTTATA CGGAGACTT ACCTTGAGAC CCAAGACCCC TCTACCGGG TTGTCAGA ATTGAGCTC ATTGCAACT CCTGTAATGC AGCAGCAGCC TCTAGAAAAA AAATGAAGC CTTTCCAT GGAGCCCATAT AACCTAAATC TATTGACA AACTCGGCAG TAACGTTGAA GGACATTAG TCGTCGTGG AGATCTTTT TTTCATTCG GAAAGGGTA CCTCGGTATA TTGTTATTAG
+3	IleLysLeuPhe GluProSer LeuGlnPro ProValMetGln GlnGlnPro LeuGluLys LysMetLysPro PheProMet GluProTyr AsnHisAsnPro
11501	ATTAACCTG TTGAGCGTC ATTGCAACT CCTGTAATGC AGCAGCAGCC TCTAGAAAAA AAATGAAGC CTTTCCAT GGAGCCCATAT AACCTAAATC TATTGACA AACTCGGCAG TAACGTTGAA GGACATTAG TCGTCGTGG AGATCTTTT TTTCATTCG GAAAGGGTA CCTCGGTATA TTGTTATTAG
+3	ProSerGluValPro GluPhyTrp AspSerSer TyrSerMet AlaAspSerArg SerValMet AlaGlnGln AlaAsnIleAsp ArgArgGly
11501	CCTCAAGCT CAAGGTCCCA GAATTCTACT GGGATCTTC CTACAGCATG GTCGTAACAA GATCGTAAT GGCACAGGAA GCAACATAG ACCGCAAGGG GGAGTCCTCA GTTCCAGGT CTTAAGATGA CCCTAAGAAG GATGTCGTAC CGACTATGT CTAGACATA CGCTGTGTT CGTTTGATTC TGGCGTCCCC
+3	GlyLysArgSer ProGlyValPhe ArgProGlu GlnAspPro ValProArgMet ProProGlu LysSerLeu LeuGluLysPro SerGluLeu MetSerHis
11501	CAACCGCTCA CCAGGAGTCT TCCGTCAGA GCAAGGATCT GTACCCAGAA TGCCGTTGA GAAATCCTTA TTGGAGAGGC CCTCGAGGT CATGTCACAT GTTTCCAGT GTTCTCAGA AGGGAGGCT CTAGCTTAGGA CAGGGCAACT CGTGGGTCTT ACGGCAAACT CTTAGGAAT AACCTCTTG GGAGTCCTGA GTACAGTGTAA
+3	SerSerSerPhe LeuSerLeu ThrglyPhe SerLeuAsnGln GluValTyr ProAsnAsn SerMetPheAsn GlnValTyr GlyLysAsn LeuThrSerSerHis
11501	TCATCCCTCT TCCTGTCCT CACGGGATTC TCTCTCAATC AGGAAAGATA CCCAAATAAT AGTATGTTCA ATGGGAAAC CTGACATCCCA AGTAGGCAAA ACCACAGGAA GTGGCCTAAG AGAGAGTTAG TCATACAAGT TACTCCATAT ACCCCATTAT GGGTTTCTAT GGTCTTTTG GACTGTAGGT
+3	SerSerSerAla GluLeuSer ProSerMetAla ProGlnGlu ThrSerLeuPhe GluGlyThr ProTrpSer ProSerLeuPro AlaSerSer
11501	GCTCCAAAGC AGAACTCTAGT CCCTCAATG cccccccAGGA AAACATCTCTG TATTCCCTTT TTGAAGGGAC TCCCTGCTCTT CCATCCTCTC CTGGCACTTC CGAGETTTTCG TCTTGAGCTCA GGGGGGTCTC TTGGTAGAGAC AACTTCCTG AGGGGACCAAGA GGTAGTGAAAG GACGGCTCAAG GACGGCTCAAG

FIG. 1D

SUBSTITUTION SHEET (RULE 26)

+3 SerAspHisSer ThrProAlaSer GlnSerPro HisSerSer AsnProSerSer LeuProSer SerProSer SerProSer ThrHisAsnHis AsnSerVal ProProSer

2201 AGATCATCA ACACCAAGCA GCGTACCCAG CTCTCTCCA ACACACAACC ATAATTCTGT TCCATCTCC
TCATGAACT TGTTGGCTGGT CGGTAGGG AGTAAGGAGA TTGGGTTCGT CGGATGGGT GAGGAGGT TTGTTGTTGG TATTAAGACA AGGTAAAGGG

+3 AsnPheGlyPro IleGlyThr ProAspSer ArgAspArg ThrAlaAsp ArgTriplys ThraspLysPro AlaMetGly GlyPheGly IleAspTyrLeu

2301 AATTGGAC CCATTGGAC TCCAGATAAC AGGGATAGAA GGACTGCGAGA TCGGTGGAAA ACTGATAAGC CAGCCATGGG TGGGTGCGC ATTGATTATC
TTAAACCTTG GGTAAACCTG AGSTCTATG TCCCTATCT AGCCACCTT AGCCACCTT TGACTATTG GTCCGTACCC ACCCAAACCC TAACTAATG

+3 LeuSerAlaThr SerSerSer GluSerSerIrp HisGlnAla SerThrPro SerGlyThrIrp ThrglyHis GlyProSer MetGluAspSer SerAlaVal

2401 TCTCAGGAAAC GTCATCTCT GAGGAGGTT GGCATCAGGC CAGGACTCTCG AGTGGCACT GGACAGGCCA TGGCCCTTC ATGGAGGATT CCTCTGCTGT
AGAGTCGTTG CAGTAGGAGA CTCTCGTCAA CCGTAGTGTCCG GTCGGTGGGGC TCAACGGTGA CCTGTCGGGT ACCGGGAAGG TACCTCTTA GAGAGGACA

+3 ValLeuMetGlu SerLeuIleSer IleItpSer SerSerMet MethItpDrolg ProSerAla LeuLeuMetGln LysGlnGln LysGlnGln

2501 CCTCATGGAA AGCTTAAGT CTATCTGGTC CAGTTCCATG ATGGCATCTG GACCTTCTGC TCTGGAGCAG CTGTTAATGC AGCGAGAGCA GAACAGCA
GGAGTACCTT TCGGATTTCA GATAGACCAAG GTCAAGGTAC TAGTGTAGGC AGACCTCGTC GACAATTACG TCGTCTCTGT CTITGCTGTT

+3 ArgGlyGlnGly ThrMetAsn ProProHis ***

2601 CGGGGAAAG GCACCATGAA CCCTCCACAC TGAGGCCAAA GTGGCAACCT GGGAAATGAG GCTCCATAA CCATGGCATG TIGGGTTGC AGGACTGGCC
GCCCTCTTC CGTGGTACTT GGGAGGTGT ACTCCGGTT CACCGTTGGA CCCTTACTTC CGAGGATTG GTTACCGTAC AACCCMAGG TCCTAACCGG
CACACATCC CCTGGAGGTG GCAGCCCTCT TTTCGTTTC TCGGTCTCA GAGGGTGTAA GTATTCCACC AGGCCGGTGA GTGTGCAAGA AATGTTGCGCA

2701 GTGTGTCAAG GGAGGTCCAC CGTCGGAGA AAAGACAAAG AGCAGACAGTT CTCCACATT CATAAGGTGG TCGGGGGAAT CACACGTGT TTACAGGGT
GTGGCAACAA AACAAAAATC CATAGAAC TCTCCGTCCC CCCGGGGCTT TCGGAGGGAGA GAGAGAGGG AACTGTGTGT TATCTCAGT AGTTACTTGG
CACCTGTTT TCTCTCTG GTAGTCCTG AGAGGAGGG GGGCCCCCGGA AGGCCTCCCT CTCTCTCTCC TTGACGACAA ATAGAGTGG AGTACGAAACC

2801 TATCACCGCC TCTCAC
ATAGAGGCGG AGAGTGG

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FIG. 2A

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FIG. 2B

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FIG. 2C

SUBSTITUTE SHEET (RUL 26)

+3	GlnGlyProLeu GlyLysIle MetProValLys GluProTyr TyrLeuGln ThrGlnAspPro IleLysLeu PheGluPro SerLeuGlnPro ProValMet
1501	AAGGCCATT AGGGAAATT ATGCCGTGTA AACACCCCTA CTACCTTCAG ACCCAAGACC CCATAAAACT GTTGGCCG TCATTCGAAC CCTCTGTAAT TTCCGGGTAAC TCCCCTTTAA TAGCGAACACT TTGTCGGGAT GATGGAAGTC TGGGTTCTGG GGTTATTGTA CAAACTGGC AGTAACGTT GAGGACATTA
+3	MetGlnGlnGln ProLeuGluLys LysMetLys ProPhePro MetGluProTyr AsnHisAsn ProSerGlu ValIysValPro GluPheTyr TrpAspSer
1601	GCAGGAGCAG CCTCTAGAAA AAAAATGAA GCCTTTCCC ATGGAGCCAT ATAACCCATAA TCCCTCAGAA GTCAAGTCC CAGAAATTCA CTGGGATTCT CGTGTGTCGTC GGAGATCTT TTTTACTT CGGAAAGGG TACCTCGGTA TATTGGTATT AGGGACTCTT CTTGGCTCAGG GTCTTAAGAT GACCCTAAGA
+3	SerTyrSerMet AlaAspAsn ArgSerVal MetAlaGlnGln AlaAsnIle AspArgArg GlyLysArgSer ProGlyVal PheArgPro GluGlnAspPro
1701	TCCTACAGCA TGCGTGATAA CAGATCTGA ATAAGCACAA AGACCAAACAT AGACCGGAGG GSCMAACGGT CACAGGAGT CTTCCTGTCGA GAAGGAGGT CTGCTCCTAG AGGATGTCG TGCGACTATT GCTCTAGACAT TACCGCTGTA TCTGGTTGTA TCTGGCTGTC CCGGTTGCCA GTGGTCTCAGA GAAGGAGGT CTGCTCCTAG
+3	ProValProArg MetProPhe GluLysSerLeu LeuGluLys ProSerGlu LeuMetSerHis SerSerSer PheLeuSer LeuThrGlyPhe SerLeuAsn
1801	CTGTACCCAG AATGCCGGTT GAGAAATCTT TATTGAGAA GCCTCTAGAG CTCATGTCAC ATTCACTCTC TTTCCTGTC CTCACCGGAT TCTCTCTCAA GACATGGGTCT TAACGGCAA CTCTTAGGA ATAACCTCTT CGGGAGTC GAGTACAGTG TAATGAGGAG AAAGGACAGG GAGTGGCTA AGAGAGAGTT
+3	AsnGlnGluArg TyrProAsnAsn SerMetPhe AsnGluVal TyrGlyLysAsn LeuThrSer SerSerLys AlaGluLeuSer ProSerMet AlaProGln
1901	TCAGGAAGA TACCCAAATA ATAGTATTT CAATGAGGTA TATGGAAAA ACCTGACAT CAGCTCCAAA GCAGAACTCA GTCCCTCAAT GGCCCCCAG AGTCCTCTTCTT ATGGGTTTAT TATCATACAA GTTACTCCAT ATTACCTTTT TGGACTGTAG GTCGAGGTTT CGTCCTGAGT CAGGGAGTTA CGGGGGGTC
+3	GlutHSerLeu TyrSerLeu PheGluLys ThrProTrpSer ProSerLeu SerAspHisSer ThrProAla SerGlnSer ProHisSerSer
2001	GAAACATCTC TGATATCCCT TTGAGGG ACTCCGTT CTCCATCACT TCAGATCATT CAAACCCAG CAGCCAGCT CCTCATTCCT CTTGTAGAG ACATAAGGAA AAAACTCCC TGAGGACCA GAGGTAGTGA AGGAGGGTCA ACTCTAGTA GTTGTGTCG GTGGGTCAAGA GGAGTAAGGA
+3	SerAsnProSer SerLeuPro SerSerProPro ThnHisAsnSer ValProPheSer AsnPheGly ProIleGly ThrProAspAsn ArgAspArg
2101	CTAACCAAG CAGCCTACCC AGCTCTCTC AGCTGATGGG TCGAGGAGG GTTGTGTTT CCAATTCTT ACCCATTGGG ACTCCAGATA ACAGGGATAG GATTGGTTC GTGGGATGGG TCGAGGAGG GTTGTGTTT GTGAGTAAGA CAAAGTAAGA GGTTATAACC TGAGGTCTAT TGTCCTATC

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FIG. 2D

+3 ArgArgThrAla AspArgTriPlys ThrAspPlys ProAlaMet GlyGlyPheGly IleAspTyr LeuSerAla ThrSerSerSer GluSerSer TrpHisGln

2201 AAGGACTGCA GATCGGTGGA AACTGATAA GCCAGCCTTG GGTTGGTTG GCATTGATA TCTCTAGCA AGTCATCCCT CTGAGACAG TTGGCATCAG TTCTGACGT CTAGCCACCT TTGACTT CGGTCGGTAC CCACCAAAC CGTAACATA AGAGTCGTG TGCGTAGGA AACCTGTGC AACCGTAGTC

+3 AlaSerThrPro SerGlyThr TrpThrGly HisGlyProSer MetGluAsp SerGluAsp SerSerAla ValLeuAla SerLeuLys SerIleTrp SerSerSerMet

2301 GCCAGCACTC CGAGTGGCAC CTGGACAGGC CATGGCCCTT CCTGGAGGA TTCCTCATGG AAAGCCTAA GTCTATCTGG TCCAGTCCA CGCTCGTGG GCTCACCGTG GACCTGTGG GACCTGGAA GTAACCTCTT AAGGAGACCA CAGGAGTACC TTICGGATT CAGATAGACC AGGTCAAGGT

+3 MetMethIlePro GlyProSer AlaLeuGluGln LysLeuMet GlnGlnLys GlnLysGlnGln ArgGlyGln GlyThrMet AsnProProHis ***

2401 TGATGCATCC TGGACCTCT GCTCTGGAGC AGCTGTTAAT GCAGAACAG CAGAAACAGC AACGGGACA AGGGGACA AGGCAACATG AACCTTCAC ACTGAGGCCA ACTACGTTG ACTTGGAAAGA CGAGACCTCG TCGACAAATA CGTGTGCTTC GTCTTGTG TTGCCCCCTGT TCCCTGCTAC TTGGAAGCTG TGCTCCGGT AAGTGGCAAC CTGGGAATGA AGGCTCCATA ACCATGGCA TGTGGGGTT GCAGGACTGG CCCAACAGT CCCCTGCAAG TGCGAGCCT CTTTCTGTT TICACCGTTG GACCCCTACT TCCGAGGTAT TTGGTACCGT ACACCCAA CGTCTGTG GGGGACGTC ACCGTGGGA GAAAGACAA TCTCGCTGTC AAGGGGTG AAGTATTCA CCAGCCCCGT GAGTGTGCAAC GAAATGTG CAGTGAACA AAAGAAAAA TCCATCGGA ACTTCGGTC AGAGGACAG TTCTCCACA TTCAAAAGT GGTGGGGCA CTACACGTT CTTAACAGTGC GTCACTAACG TCAGTGTGT TTTCCTGTT AGGTGTTCT TGAGGGCAG CCCCGGGGC CTTCGGAGG GAGAGAGAGA CGAACCTGG TGTTATCTCAC TCAGTACTT GGTATCACCG CCTCTCACCG GGGGGCCCG GAAGGGCCCG CTCTCTCTCT CCATAGTGGC CCATAGTGGC GGAGAGTGG

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FIG. 3

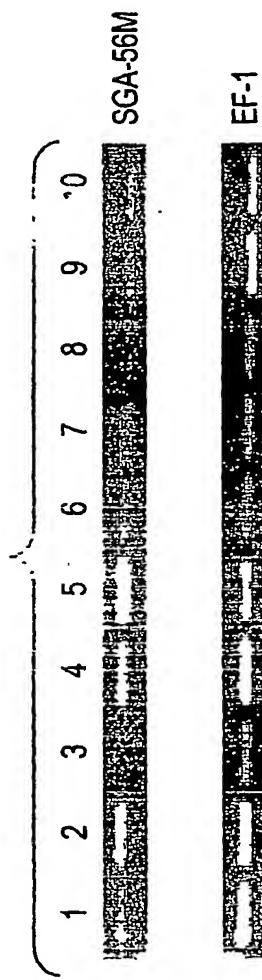
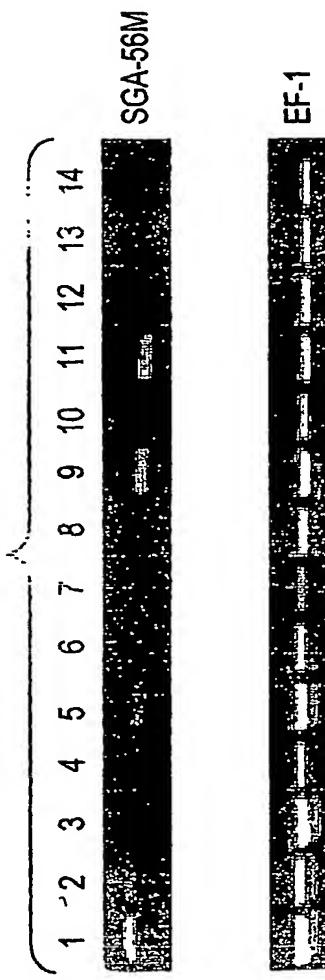


FIG. 4



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FIG. 5A

	1	2	3	4	5	6	7	8	9	10	11
A
B
C
D
E
F
G
H

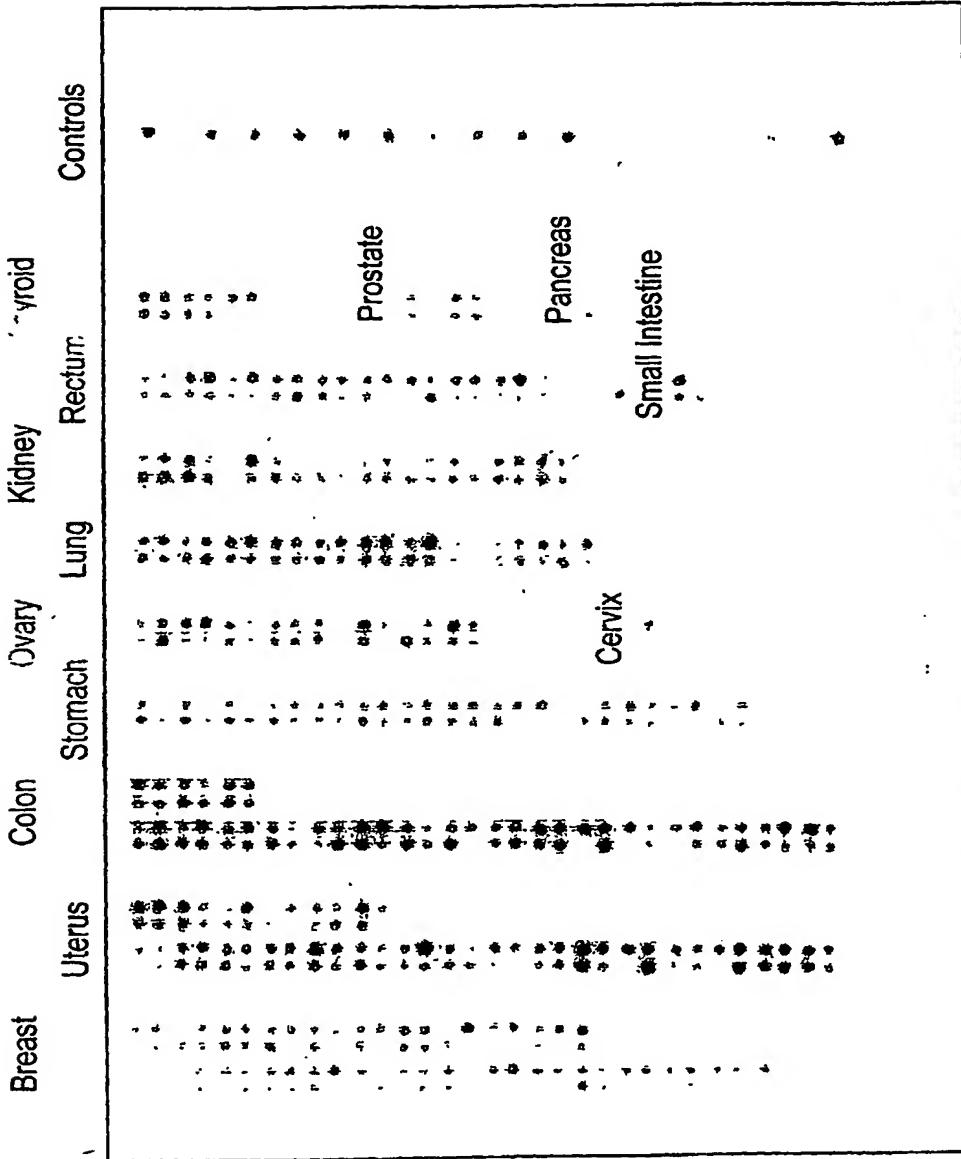
FIG. 5B

	1	2	3	4	5	6	7	8	9	10	11
A											
B											
C											
D											
E											
F											
G											
H											

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FIG. 6



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FIG. 7

1 MSFLGILCKC PLQNESQEES YNAYPLPAVK VSMDWLRLRP RVFQEAVVDE
 51 RQYIWPWLIS LLNSFHPHEE DLSSISATPL PEEFELQGFL ALRPSFRNLD
 101 FSKGHQGITG DKEGQQRIR QRQLISIGKW IADNQPRLIQ CENEVGKLLF
 151 ITEIPELILE DPSEAKENLI LQETSVIESL AADGSPGLKS VLSTSRNLSN
 201 NCDTGEKPVV TFKENIKTRE VNRDQGRSFP PKEVRRDYSK GITVTKNDGK
 251 KDNNKRKTET KKCTLEKLQE TGKQNVAQV KSQTELRKTP VSEARKTPVT
 301 QTPTQASNSQ FIFIHHPGAF PPLPSRPGF PPTYVIPPPV AFMSGSGYTF
 351 PAGVSVPGTF LQPTAHSPAG NQVQAGKQSH IPYSQQRPSG PGPMNQGPQQ
 401 SQPPSQQPLT SLPAQPTAQ TSQQLQVQALT QQQQSPTKAV PALGKSPPHH
 451 SGFQQYQQAD ASKQLWNPPQ VQGPLGKIMP VKQPYYLQTO DPIKLFEPSL
 501 QPPVMQQQPL EKKMKPFPM E PYNHNPSVEK VPEFYWDSSY SMADNRSVMA
 551 QQANIDRRGK RSPGVFRPEQ DPVPRMPFEK SLLEKPSELM SHSSSFLSLT
 601 GFSLNQERYP NNSMFNEVYG KNLTSSKAE LSPSMAPQET SLYSLFEGTP
 651 WSPSLPASSD HSTPASQSPH SSNPSSLPSS PPTHNHNSVP FSNGFGPIGTP
 701 DNDRRTADR WKTDKPAAMGG FGIDYLSATS SSESSWHQAS TPSGTWTGHG
 751 PSMEDSSAVL MESLKSIWSS SMMHPGPSAL EQLLMQQKQK QQRGQGTMNP
 801 PH

FIG. 8

1 MSFLGILCKC PLQNESQEES YNAYPLPAVK VSMDWLRLRP RVFQEAVVDE
 51 RQYIWPWLIS LLNSFHPHEE DLSSISATPL PEEFELQGFL ALRPSFRNLD
 101 FSKGHQGITG DKEGQQRIR QRQLISIGKW IADNQPRLIQ CENEVGKLLF
 151 ITEIPELILE DPSEAKENLI LQETSVIESL AADGSPGLKS VLSTSRNLSN
 201 NCDTGEKPVV TFKENIKTRE VNRDQGRSFP PKEVKSQTGL RKTPVSEARK
 251 TPVTQPTQA SNSQFIPIH PGAFPPLPSR PGFPPTYVI PPPVAFSMGS
 301 GYTFPAGVSV PGTFLQPTAH SPAGNQVQAG KQSHIPYSQQ RPSGPGPMMQ
 351 GPQQSQPPSQ QPLTSLPAQP TAQSTSSQLQV QALTQQQQSP TKAVPALGKS
 401 PPHHSGFQQY QQADASKQLW NPPQVQGPLG KIMPVKQPY LQTQDPPIKLF
 451 EPSLQPPVMQ QQPLEKKMKP FPMEPYNHNP SEVKVPEFYW DSSYSMADNR
 501 SVMAQQANID RRGKRSQGVF RPEQDPVPRM PFEKSLLEKP SELMSHSSSF
 551 LS LTGFSLNQ ERYPNNSMFN EVYGKNLTSS SKAELSPSMA PQETSLYSLF
 601 EGTPWSPSLP ASSDHSTPAS QSPHSSNPSS LPSSPPTHNH NSVPFSNFGP
 651 IGTPDNRDRR TADRWKTDKP AMGGFGIDYL SATSSSESSW HQASTPSGTW
 701 TGHGPSMEDS SAVLMESLKS IWSSSMMHPG PSALEQLLMQ QKQKQQRGQG
 751 TMNPPH

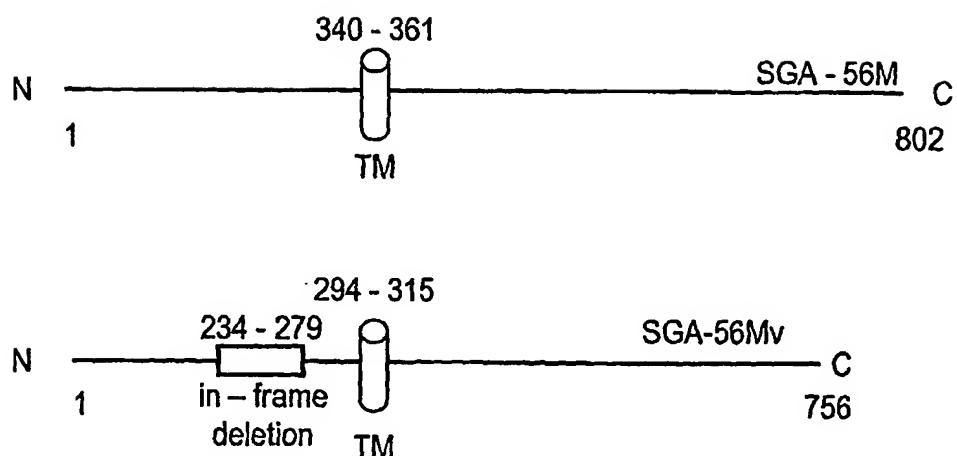
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FIG. 9



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